

SEQUENCE LISTING

<110> Centre National de la Recherche Scientifique

<120> Human TREK2, a novel stretch- and arachidonic acid-sensitive K⁺ channel activated by inhalational anesthetics and riluzole

<130> 8606PCT

<140> 8606PCT

<141> 2001-06-27

<150> US 60/214.559

<151> 2000-06-27

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 1614

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1614)

<223> ORF of human TREK2 cDNA

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gca gca gca ccg gtg tgc cag ccc aag agc gcc act aac ggg caa ccc 96

Ala Ala Ala Pro Val Cys Gln Pro Lys Ser Ala Thr Asn Gly Gln Pro

20 25 30

ccg gct ccg gct ccg act cca act ccg cgc ctg tcc att tcc tcc cga 144

Pro Ala Pro Ala Pro Thr Pro Thr Pro Arg Leu Ser Ile Ser Ser Arg

35 40 45

gcc aca gtg gta gcc agg atg gaa ggc acc tcc caa ggg ggc ttg cag 192

Ala Thr Val Val Ala Arg Met Glu Gly Thr Ser Gln Gly Gly Leu Gln

50 55 60

acc gtc atg aag tgg aag acg gtg gtt gcc atc ttt gtg gtt gtg gtg 240

Thr Val Met Lys Trp Lys Thr Val Val Ala Ile Phe Val Val Val Val

65 70 75 80

gtc tac ctt gtc act ggc ggt ctt gtc ttc cgg gca ttg gag cag ccc 288

Val Tyr Leu Val Thr Gly Gly Leu Val Phe Arg Ala Leu Glu Gln Pro

85 90 95

ttt gag agc agc cag aag aat acc atc gcc ttg gag aag gcg gaa ttc 336

Phe Glu Ser Ser Gln Lys Asn Thr Ile Ala Leu Glu Lys Ala Glu Phe

100 105 110

ctg cgg gat cat gtc tgt gtg agc ccc cag gag ctg gag acg ttg atc 384

Leu Arg Asp His Val Cys Val Ser Pro Gln Glu Leu Glu Thr Leu Ile

115 120 125

cag cat gct ctt gat gct gac aat gcg gga gtc agt cca ata gga aac Gln His Ala Leu Asp Ala Asp Asn Ala Gly Val Ser Pro Ile Gly Asn 130 135 140	432
tct tcc aac aac agc agc cac tgg gac ctc ggc agt gcc ttt ttc ttt Ser Ser Asn Asn Ser Ser His Trp Asp Leu Gly Ser Ala Phe Phe Phe 145 150 155 160	480
gct gga act gtc att acg acc ata ggg tat ggg aat att gct ccg agc Ala Gly Thr Val Ile Thr Thr Ile Gly Tyr Gly Asn Ile Ala Pro Ser 165 170 175	528
act gaa gga ggc aaa atc ttt tgt att tta tat gcc atc ttt gga att Thr Glu Gly Gly Lys Ile Phe Cys Ile Leu Tyr Ala Ile Phe Gly Ile 180 185 190	576
cca ctc ttt ggt ttc tta ttg gct gga att gga gac caa ctt gga acc Pro Leu Phe Gly Phe Leu Leu Ala Gly Ile Gly Asp Gln Leu Gly Thr 195 200 205	624
atc ttt ggg aaa agc att gca aga gtg gag aag gtc ttt cga aaa aag Ile Phe Gly Lys Ser Ile Ala Arg Val Glu Lys Val Phe Arg Lys Lys 210 215 220	672
caa gtg agt cag acc aag atc cgg gtc atc tca acc atc ctg ttc atc Gln Val Ser Gln Thr Lys Ile Arg Val Ile Ser Thr Ile Leu Phe Ile 225 230 235 240	720
ttg gcc ggc tgc att gtg ttt gtg acg atc cct gct gtc atc ttt aag Leu Ala Gly Cys Ile Val Phe Val Thr Ile Pro Ala Val Ile Phe Lys 245 250 255	768
tac atc gag ggc tgg acg gcc ttg gag tcc att tac ttt gtg gtg gtc Tyr Ile Glu Gly Trp Thr Ala Leu Glu Ser Ile Tyr Phe Val Val Val 260 265 270	816
act ctg acc acg gtg ggc ttt ggt gat ttt gtg gca ggg gga aac gct Thr Leu Thr Thr Val Gly Phe Gly Asp Phe Val Ala Gly Gly Asn Ala 275 280 285	864
ggc atc aat tat cgg gag tgg tat aag ccc cta gtg tgg ttt tgg atc Gly Ile Asn Tyr Arg Glu Trp Tyr Lys Pro Leu Val Trp Phe Trp Ile 290 295 300	912
ctt gtt ggc ctt gcc tac ttt gca gct gtc ctc agt atg atc gga gat Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu Ser Met Ile Gly Asp 305 310 315 320	960
tgg cta cgg gtt ctg tcc aaa aag aca aaa gaa gag gtg ggt gaa atc Trp Leu Arg Val Leu Ser Lys Lys Thr Lys Glu Glu Val Gly Glu Ile 325 330 335	1008
aag gcc cat gcg gca gag tgg aag gcc aat gtc acg gct gag ttc cgg Lys Ala His Ala Ala Glu Trp Lys Ala Asn Val Thr Ala Glu Phe Arg 340 345 350	1056
gag aca cgg cga agg ctc agc gtg gag atc cac gat aag ctg cag cgg Glu Thr Arg Arg Arg Leu Ser Val Glu Ile His Asp Lys Leu Gln Arg 355 360 365	1104

gcg gcc acc atc cgc agc atg gag cgc cgg cgg ctg ggc ctg gac cag 1152
Ala Ala Thr Ile Arg Ser Met Glu Arg Arg Arg Leu Gly Leu Asp Gln
370 375 380

cgg gcc cac tca ctg gac atg ctg tcc ccc gag aag cgc tct gtc ttt 1200
Arg Ala His Ser Leu Asp Met Leu Ser Pro Glu Lys Arg Ser Val Phe
385 390 395 400

gct gcc ctg gac acc ggc cgc ttc aag gcc tca tcc cag gag agc atc 1248
Ala Ala Leu Asp Thr Gly Arg Phe Lys Ala Ser Ser Gln Glu Ser Ile
405 410 415

aac aac cgg ccc aac aac ctg cgc ctg aag ggg cgg gag cag ctg aac 1296
Asn Asn Arg Pro Asn Asn Leu Arg Leu Lys Gly Pro Glu Gln Leu Asn
420 425 430

aag cat ggg cag ggt gcg tcc gag gac aac atc atc aac aag ttc ggg 1344
Lys His Gly Gln Gly Ala Ser Glu Asp Asn Ile Ile Asn Lys Phe Gly
435 440 445

tcc acc tcc aga ctc acc aag agg aaa aac aag gac ctc aaa aag acc 1392
Ser Thr Ser Arg Leu Thr Lys Arg Lys Asn Lys Asp Leu Lys Lys Thr
450 455 460

ttg ccc gag gac gtt cag aaa atc tac aag acc ttc cgg aat tac tcc 1440
Leu Pro Glu Asp Val Gln Lys Ile Tyr Lys Thr Phe Arg Asn Tyr Ser
465 470 475 480

ctg gac gag gag aag aaa gag gag gag acg gaa aag atg tgt aac tca 1488
Leu Asp Glu Glu Lys Lys Glu Glu Glu Thr Glu Lys Met Cys Asn Ser
485 490 495

gac aac tcc agc aca gcc atg ctg acg gac tgt atc cag cag cac gct 1536
Asp Asn Ser Ser Thr Ala Met Leu Thr Asp Cys Ile Gln Gln His Ala
500 505 510

gag ttg gag aac gga atg ata ccc acg gac acc aaa gac cgg gag ccg 1584
Glu Leu Glu Asn Gly Met Ile Pro Thr Asp Thr Lys Asp Arg Glu Pro
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gag aac aac tca tta ctt gaa gac aga aac 1614
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<212> PRT
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Ala Ala Ala Pro Val Cys Gln Pro Lys Ser Ala Thr Asn Gly Gln Pro
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Pro Ala Pro Ala Pro Thr Pro Thr Pro Arg Leu Ser Ile Ser Ser Arg

35

40

45

Ala Thr Val Val Ala Arg Met Glu Gly Thr Ser Gln Gly Gly Leu Gln
 50 55 60

Thr Val Met Lys Trp Lys Thr Val Val Ala Ile Phe Val Val Val Val
 65 70 75 80

Val Tyr Leu Val Thr Gly Gly Leu Val Phe Arg Ala Leu Glu Gln Pro
 85 90 95

Phe Glu Ser Ser Gln Lys Asn Thr Ile Ala Leu Glu Lys Ala Glu Phe
 100 105 110

Leu Arg Asp His Val Cys Val Ser Pro Gln Glu Leu Glu Thr Leu Ile
 115 120 125

Gln His Ala Leu Asp Ala Asp Asn Ala Gly Val Ser Pro Ile Gly Asn
 130 135 140

Ser Ser Asn Asn Ser Ser His Trp Asp Leu Gly Ser Ala Phe Phe Phe
 145 150 155 160

Ala Gly Thr Val Ile Thr Thr Ile Gly Tyr Gly Asn Ile Ala Pro Ser
 165 170 175

Thr Glu Gly Gly Lys Ile Phe Cys Ile Leu Tyr Ala Ile Phe Gly Ile
 180 185 190

Pro Leu Phe Gly Phe Leu Leu Ala Gly Ile Gly Asp Gln Leu Gly Thr
 195 200 205

Ile Phe Gly Lys Ser Ile Ala Arg Val Glu Lys Val Phe Arg Lys Lys
 210 215 220

Gln Val Ser Gln Thr Lys Ile Arg Val Ile Ser Thr Ile Leu Phe Ile
 225 230 235 240

Leu Ala Gly Cys Ile Val Phe Val Thr Ile Pro Ala Val Ile Phe Lys
 245 250 255

Tyr Ile Glu Gly Trp Thr Ala Leu Glu Ser Ile Tyr Phe Val Val Val
 260 265 270

Thr Leu Thr Thr Val Gly Phe Gly Asp Phe Val Ala Gly Gly Asn Ala

275 280 285
 Gly Ile Asn Tyr Arg Glu Trp Tyr Lys Pro Leu Val Trp Phe Trp Ile
 290 295 300
 Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu Ser Met Ile Gly Asp
 305 310 315 320
 Trp Leu Arg Val Leu Ser Lys Lys Thr Lys Glu Glu Val Gly Glu Ile
 325 330 335
 Lys Ala His Ala Ala Glu Trp Lys Ala Asn Val Thr Ala Glu Phe Arg
 340 345 350
 Glu Thr Arg Arg Arg Leu Ser Val Glu Ile His Asp Lys Leu Gln Arg
 355 360 365
 Ala Ala Thr Ile Arg Ser Met Glu Arg Arg Arg Leu Gly Leu Asp Gln
 370 375 380
 Arg Ala His Ser Leu Asp Met Leu Ser Pro Glu Lys Arg Ser Val Phe
 385 390 395 400
 Ala Ala Leu Asp Thr Gly Arg Phe Lys Ala Ser Ser Gln Glu Ser Ile
 405 410 415
 Asn Asn Arg Pro Asn Asn Leu Arg Leu Lys Gly Pro Glu Gln Leu Asn
 420 425 430
 Lys His Gly Gln Gly Ala Ser Glu Asp Asn Ile Ile Asn Lys Phe Gly
 435 440 445
 Ser Thr Ser Arg Leu Thr Lys Arg Lys Asn Lys Asp Leu Lys Lys Thr
 450 455 460
 Leu Pro Glu Asp Val Gln Lys Ile Tyr Lys Thr Phe Arg Asn Tyr Ser
 465 470 475 480
 Leu Asp Glu Glu Lys Lys Glu Glu Glu Thr Glu Lys Met Cys Asn Ser
 485 490 495
 Asp Asn Ser Ser Thr Ala Met Leu Thr Asp Cys Ile Gln Gln His Ala
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515

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 <223> Antisense primer for 5'-RACE
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 <223> Sense primer for 3'-RACE
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 <222> (1)..(23)
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23

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22

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 <223> Anchor primer for RACE reaction
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 <223> TREK2 sense primer
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19

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21

<210> 11
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 <212> DNA
 <213> unidentified
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 <222> (1)..(22)
 <223> TRAAK sense primer
 <400> 11
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22

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 <223> TRAAK antisense primer
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 <223> TREK1 sense primer
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 <222> (1)..(20)
 <223> TREK1 antisense primer
 <400> 14
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<210> 15
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 <222> (1)..(27)
 <223> 32P-labeled primer (TREK2)
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<210> 16
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 <212> DNA
 <213> unidentified
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 <223> 32P-labeled primer (TRAAK)
 <400> 16
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<210> 17
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tagctgatct ccaactccag ccaag

25

tagctgatct ccaactccag ccaag